SEQUENCE LISTING

<110> Maines, Mahin D.

<120> METHODS OF MODIFYING CELL STRUCTURE AND REMODELING
     TISSUE

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<150> 60/261,500
<151> 2001-01-12

<160> 17

<170> PatentIn Ver. 2.1

<210> 1
<211> 296
<212> PRT
<213> Homo sapiens

<400> 1
Met Asn Ala Glu Pro Glu Arg Lys Phe Gly Val Val Val Val Gly Val
 1   5   10   15

Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
             20   25   30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
         35   40   45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
     50   55   60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
 65   70   75   80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
                 85   90   95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
             100   105   110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
         115   120   125

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Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
    130                 135                 140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ser Asp Pro Leu Glu Glu Asp
145                 150                 155                 160

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
                165                 170                 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
                180                 185                 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
                195                 200                 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
    210                 215                 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
225                 230                 235                 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
                245                 250                 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
                260                 265                 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
    275                 280                 285

Gln Lys Tyr Cys Cys Ser Arg Lys
    290                 295


<210> 2
<211> 1070
<212> DNA
<213> Homo sapiens

<400> 2
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tccgtgcgga tgagggactt gcggaatcca caccccttcct cagcgttcct gaacctgatt 180
ggcttcgtgt cgagaaggga gctcgggagc attgatggag tccagcagat ttctttggag 240
gatgctcttt ccagccaaga ggtggaggtc gcctatatct gcagtgagag ctccagccat 300
gaggactaca tcaggcagtt ccttaatgct ggcaagcacg tccttgtgga ataccccatg 360
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2

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cggtttggct ccctgcatt cagcggcatc tctcgactga cctggctggt ctccctcttt 600
ggggagcttt ctcttgtgtc tgccactttg gaagagcgaa aggaagatca gtatatgaaa 660
atgacagtgt gtctggagac agagaagaaa agtccactgt catggattga agaaaaagga 720
cctggtctaa aacgaaacag atatttaagc ttccatttca gtctgggtc cttggagaat 780
gtgccaaatg taggagtgaa taagaacata tttctgaaag atcaaaatat atttgtccag 840
aaactcttgg gccagttctc tgagaaggaa ctggctgctg aaaagaaacg catcctgcac 900
tgcctggggc ttgcagaaga aatccagaaa tattgctgtt caaggaagta agaggaggag 960
gtgatgtagc acttccaaga tggcaccagc atttggttct tctcaagagt tgaccattat 1020
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<210> 3
<211> 296
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<213> Homo sapiens

<400> 3
Met Asn Thr Glu Pro Glu Arg Lys Phe Gly Val Val Val Gly Val
1   5   10   15

Gly Arg Ala Gly Ser Val Arg Met Arg Asp Leu Arg Asn Pro His Pro
        20   25   30

Ser Ser Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu
        35   40   45

Gly Ser Ile Asp Gly Val Gln Gln Ile Ser Leu Glu Asp Ala Leu Ser
    50   55   60

Ser Gln Glu Val Glu Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His
65   70   75   80

Glu Asp Tyr Ile Arg Gln Phe Leu Asn Ala Gly Lys His Val Leu Val
                85   90   95

Glu Tyr Pro Met Thr Leu Ser Leu Ala Ala Ala Gln Glu Leu Trp Glu
            100   105   110

Leu Ala Glu Gln Lys Gly Lys Val Leu His Glu Glu His Val Glu Leu
        115   120   125

Leu Met Glu Glu Phe Ala Phe Leu Lys Lys Glu Val Val Gly Lys Asp
        130   135   140

Leu Leu Lys Gly Ser Leu Leu Phe Thr Ala Gly Pro Leu Glu Glu Glu
145   150   155   160
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3

Arg Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu
                165                 170                 175

Val Ser Leu Phe Gly Glu Leu Ser Leu Val Ser Ala Thr Leu Glu Glu
                180                 185                 190

Arg Lys Glu Asp Gln Tyr Met Lys Met Thr Val Cys Leu Glu Thr Glu
                195                 200                 205

Lys Lys Ser Pro Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys
            210                 215                 220

Arg Asn Arg Tyr Leu Ser Phe His Phe Lys Ser Gly Ser Leu Glu Asn
        225                 230                 235                 240

Val Pro Asn Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asn
                245                 250                 255

Ile Phe Val Gln Lys Leu Leu Gly Gln Phe Ser Glu Lys Glu Leu Ala
                260                 265                 270

Ala Glu Lys Lys Arg Ile Leu His Cys Leu Gly Leu Ala Glu Glu Ile
            275                 280                 285

Gln Lys Tyr Cys Cys Ser Arg Lys
        290                 295


<210> 4
<211> 295
<212> PRT
<213> Rattus norvegicus

<400> 4
Met Asp Ala Glu Pro Lys Arg Lys Phe Gly Val Val Val Val Gly Val
1               5                   10                  15

Gly Arg Ala Gly Ser Val Arg Leu Arg Asp Leu Lys Asp Pro Arg Ser
            20                  25                  30

Ala Ala Phe Leu Asn Leu Ile Gly Phe Val Ser Arg Arg Glu Leu Gly
        35                  40                  45

Ser Leu Asp Glu Val Arg Gln Ile Ser Leu Glu Asp Ala Leu Arg Ser
        50                  55                  60

Gln Glu Ile Asp Val Ala Tyr Ile Cys Ser Glu Ser Ser Ser His Glu

4

Asp Tyr Ile Arg Gln Phe Leu Gln Ala Gly Lys His Val Leu Val Glu
                    85                  90                  95

Tyr Pro Met Thr Leu Ser Phe Ala Ala Ala Gln Glu Leu Trp Glu Leu
                100                 105                 110

Ala Ala Gln Lys Gly Arg Val Leu His Glu Glu His Val Glu Leu Leu
            115                 120                 125

Met Glu Glu Phe Glu Phe Leu Arg Arg Glu Val Leu Gly Lys Glu Leu
        130                 135                 140

Leu Lys Gly Ser Leu Arg Phe Thr Ala Ser Pro Leu Glu Glu Glu Arg
145                 150                 155                 160

Phe Gly Phe Pro Ala Phe Ser Gly Ile Ser Arg Leu Thr Trp Leu Val
                165                 170                 175

Ser Leu Phe Gly Glu Leu Ser Leu Ile Ser Ala Thr Leu Glu Glu Arg
                180                 185                 190

Lys Glu Asp Gln Tyr Met Lys Met Thr Val Gln Leu Glu Thr Gln Asn
            195                 200                 205

Lys Gly Leu Leu Ser Trp Ile Glu Glu Lys Gly Pro Gly Leu Lys Arg
        210                 215                 220

Asn Arg Tyr Val Asn Phe Gln Phe Thr Ser Gly Ser Leu Glu Glu Val
225                 230                 235                 240

Pro Ser Val Gly Val Asn Lys Asn Ile Phe Leu Lys Asp Gln Asp Ile
                245                 250                 255

Phe Val Gln Lys Leu Leu Asp Gln Val Ser Ala Glu Asp Leu Ala Ala
            260                 265                 270

Glu Lys Lys Arg Ile Met His Cys Leu Gly Leu Ala Ser Asp Ile Gln
        275                 280                 285

Lys Leu Cys His Gln Lys Lys
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<210> 5
<211> 1081
<212> DNA

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<213> Rattus norvegicus

<400> 5
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gaaatttgga gtggtagtgg ttggtgttgg cagagctggc tcggtgaggc tgagggactt 180
gaaggatcca cgctctgcag cattcctgaa cctgattgga tttgtgtcca gacgagagct 240
tgggagcctt gatgaagtac ggcagatttc tttggaagat gctctccgaa gccaagagat 300
tgatgtcgcc tatatttgca gtgagagttc cagccatgaa gactatatac ggcagtttct 360
gcaggctggc aagcatgtcc tcgtggaata ccccatgaca ctgtcatttg cggcggccca 420
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gtctcttcgc ttcacagcta gcccactgga agaagagaga tttggcttcc ctgcgttcag 600
cggcatttct cgcctgacct ggctggtctc cctcttcggg gagctttctc ttatttctgc 660
caccttggaa gagcgaaaag aggatcagta tatgaaaatg accgtgcagc tggagaccca 720
gaacaagggt ctgctgtcat ggattgaaga gaaagggcct ggcttaaaaa gaaacagata 780
tgtaaacttc cagttcactt ctgggtccct ggaggaagtg ccaagtgtag gggtcaataa 840
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agaggacctg gctgctgaga agaagcgcat catgcattgc ctggggctgg ccagcgacat 960
ccagaagctt tgccaccaga agaagtgaag aggaagcttc agagacttct gaagggggcc 1020
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<210> 6
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   hydrophobic
     domain of BVR

<220>
<221> PEPTIDE
<222> (2)
<223> where X is any aa

<400> 6
Phe Xaa Val Val Val Val
  1               5


<210> 7
<211> 6
<212> PRT
<213> Artificial Sequence

6.

<220>
<223> Description of Artificial Sequence: nucleotide
      binding domain of BVR

<220>
<221> PEPTIDE
<222> (2)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (4)..(5)
<223> where X is any aa

<400> 7
Gly Xaa Gly Xaa Xaa Gly
  1                 5


<210> 8
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
      oxidoreductase domain of BVR

<400> 8
Ala Gly Leu His Val Leu Val Glu
  1                 5


<210> 9
<211> 29
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: leucine
      zipper of BVR

<220>
<221> PEPTIDE
<222> (2)..(7)
<223> where X is any aa

<220>

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<221> PEPTIDE
<222> (9)..(14)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (16)..(21)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (23)..(28)
<223> where X is any aa

<400> 9
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1               5                   10                  15

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa Xaa Xaa Xaa Xaa Leu
                20                  25


<210> 10
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   kinase motif
      of BVR

<400> 10
Ser Arg Arg
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<210> 11
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   kinase motif
      of BVR

<400> 11
Lys Gly Ser
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<210> 12
<211> 3
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   kinase motif
      of BVR

<220>
<221> PEPTIDE
<222> (3)
<223> where X is any aa

<400> 12
Phe Thr Xaa
  1


<210> 13
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   nuclear
      localization signal of BVR

<400> 13
Gly Leu Lys Arg Asn Arg Tyr
  1               5


<210> 14
<211> 5
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   methylation
      site of BVR

<400> 14
Pro Gly Leu Lys Arg
  1               5
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<210> 15
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   zinc finger
      domain of BVR

<220>
<221> PEPTIDE
<222> (3)..(12)
<223> where X is any aa

<400> 15
His Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Cys
 1               5                  10


<210> 16
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   protein
      kinase C enhancing domain

<220>
<221> PEPTIDE
<222> (5)
<223> where X is any aa

<400> 16
Lys Lys Arg Ile Xaa His Cys
 1               5


<210> 17
<211> 8
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:   protein
      kinase C inhibiting domain
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<220>
<221> PEPTIDE
<222> (3)
<223> where X is any aa

<220>
<221> PEPTIDE
<222> (5)..(7)
<223> where X is any aa

<400> 17
Gln Lys Xaa Cys Xaa Xaa Xaa Lys
 1   5